

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/531,848
Source: IFWP
Date Processed by STIC: 8/15/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>10/531,848</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ___ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ___ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 ___ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 ___ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 ___ Variable Length	Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ___ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 ___ Skipped Sequences (OLD RULES)	Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 ___ Skipped Sequences (NEW RULES)	Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 ___ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents.	
10 ___ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)	
11 ___ Use of <220>	Sequence(s) ___ missing the <220> "Feature" and associated <u>numeric identifiers and responses</u> . Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules	
12 ___ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ___ Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFWP

RAW SEQUENCE LISTING

DATE: 08/15/2006

PATENT APPLICATION: US/10/531,848

TIME: 12:22:54

Input Set : A:\Sequence Listing.ST25.txt

Output Set: N:\CRF4\08152006\J531848.raw

3 <110> APPLICANT: Fu, Guoliang
 5 <120> TITLE OF INVENTION: COMBINED EXPONENTIAL AND LINEAR AMPLIFICATION
 7 <130> FILE REFERENCE: 60204.7USWO
 9 <140> CURRENT APPLICATION NUMBER: US 10/531,848
 10 <141> CURRENT FILING DATE: 2005-04-18
 12 <150> PRIOR APPLICATION NUMBER: PCT/GB2003/004794
 13 <151> PRIOR FILING DATE: 2003-10-29
 15 <150> PRIOR APPLICATION NUMBER: GB 0230238.8
 16 <151> PRIOR FILING DATE: 2002-12-28
 18 <150> PRIOR APPLICATION NUMBER: US 60/421,765
 19 <151> PRIOR FILING DATE: 2002-10-29
 21 <160> NUMBER OF SEQ ID NOS: 16
 23 <170> SOFTWARE: PatentIn version 3.3
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 68
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Synthetic probe
 33 <400> SEQUENCE: 1
 34 ccggagacgt cgttgtagct agcctgcgtc saacaagccs ggctttgcac atgccggaga 60
 36 cgtcgttg 68
 39 <210> SEQ ID NO: 2
 40 <211> LENGTH: 17
 41 <212> TYPE: DNA
 42 <213> ORGANISM: Artificial Sequence
 44 <220> FEATURE:
 45 <223> OTHER INFORMATION: Synthetic probe
 47 <400> SEQUENCE: 2
 48 ccggagacga ugcgtca 17
 51 <210> SEQ ID NO: 3
 52 <211> LENGTH: 76
 53 <212> TYPE: DNA
 54 <213> ORGANISM: Artificial Sequence
 56 <220> FEATURE:
 57 <223> OTHER INFORMATION: Synthetic probe
 60 <220> FEATURE:
 61 <221> NAME/KEY: misc_feature *misuse of 'S'*
 62 <222> LOCATION: (46)..(46)
 63 <223> OTHER INFORMATION: s is phosphorothioate linkage
 65 <220> FEATURE:
 66 <221> NAME/KEY: misc_feature
 67 <222> LOCATION: (48)..(48)

*see
pg 1-5*

**Does Not Comply
Corrected Diskette Needed**

*Per sequence rules, 'S' can
only
represent
'C' or 'G'*

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68 <223> OTHER INFORMATION: s is phosphorothioate linkage *same error*
 70 <400> SEQUENCE: 3
 71 ccggagacgt cggtgtagct agcctgcgctc aggatgcagc agcttststct tgaagagcaa 60
 73 accggagacg tcgttg 76
 76 <210> SEQ ID NO: 4
 77 <211> LENGTH: 77
 78 <212> TYPE: DNA
 79 <213> ORGANISM: Artificial Sequence
 81 <220> FEATURE:
 82 <223> OTHER INFORMATION: Synthetic probe
 85 <220> FEATURE:
 86 <221> NAME/KEY: misc_feature
 87 <222> LOCATION: (77)..(77)
 88 <223> OTHER INFORMATION: n is 3' phosphate
 90 <400> SEQUENCE: 4
 91 ccggagacgt cggtgtagct agcctgcgctc aggatgcagc agcttststct taaagagcaa 60
 W--> 93 accggagacg tcgttgn 77
 96 <210> SEQ ID NO: 5
 97 <211> LENGTH: 43
 98 <212> TYPE: DNA
 99 <213> ORGANISM: Mus musculus
 102 <220> FEATURE:
 103 <221> NAME/KEY: misc_feature
 104 <222> LOCATION: (43)..(43)
 105 <223> OTHER INFORMATION: n is 3' phosphate *same error*
 107 <400> SEQUENCE: 5
 W--> 108 ccggtttgct cttcaagaaa gctgtgcccc agaacaccag agn 43
 111 <210> SEQ ID NO: 6
 112 <211> LENGTH: 43
 113 <212> TYPE: DNA
 114 <213> ORGANISM: Mus musculus
 117 <220> FEATURE:
 118 <221> NAME/KEY: misc_feature
 119 <222> LOCATION: (43)..(43)
 120 <223> OTHER INFORMATION: n is 3' phosphate *same*
 122 <400> SEQUENCE: 6
 W--> 123 ccggtttgct ctttaagaaa gctgtgcccc agaacaccag agn 43
 126 <210> SEQ ID NO: 7
 127 <211> LENGTH: 23
 128 <212> TYPE: DNA
 129 <213> ORGANISM: Artificial Sequence
 131 <220> FEATURE:
 132 <223> OTHER INFORMATION: Artificial primer
 134 <400> SEQUENCE: 7
 135 ctctggtggt ctggggcact gca 23
 138 <210> SEQ ID NO: 8
 139 <211> LENGTH: 70
 140 <212> TYPE: DNA
 141 <213> ORGANISM: Artificial Sequence

"n" can only represent
 a single nucleotide, nothing
 else

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Input Set : A:\Sequence Listing.ST25.txt

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143 <220> FEATURE:
144 <223> OTHER INFORMATION: Artificial probe
147 <220> FEATURE:
148 <221> NAME/KEY: misc_feature
149 <222> LOCATION: (5)..(5) ✓
150 <223> OTHER INFORMATION: n can be t or u
152 <220> FEATURE:
153 <221> NAME/KEY: misc_feature
154 <222> LOCATION: (14)..(14) ✓
155 <223> OTHER INFORMATION: n can be t or u
157 <220> FEATURE:
158 <221> NAME/KEY: misc_feature
159 <222> LOCATION: (18)..(18) ✓
160 <223> OTHER INFORMATION: n can be t or u
162 <220> FEATURE:
163 <221> NAME/KEY: misc_feature
164 <222> LOCATION: (20)..(20) ✓
165 <223> OTHER INFORMATION: n can be t or u
167 <220> FEATURE:
168 <221> NAME/KEY: misc_feature ✓
169 <222> LOCATION: (23)..(23)
170 <223> OTHER INFORMATION: n can be t or u
172 <220> FEATURE:
173 <221> NAME/KEY: misc_feature ✓
174 <222> LOCATION: (27)..(27)
175 <223> OTHER INFORMATION: n can be t or u
177 <220> FEATURE:
178 <221> NAME/KEY: misc_feature
179 <222> LOCATION: (30)..(30) ✓
180 <223> OTHER INFORMATION: n can be t or u
182 <220> FEATURE:
183 <221> NAME/KEY: misc_feature
184 <222> LOCATION: (32)..(33) ✓
185 <223> OTHER INFORMATION: n can be t or u
187 <220> FEATURE:
188 <221> NAME/KEY: misc_feature
189 <222> LOCATION: (42)..(44)
190 <223> OTHER INFORMATION: n can be t or u
192 <220> FEATURE:
193 <221> NAME/KEY: misc_feature *enu*
194 <222> LOCATION: (49)..(49)
195 <223> OTHER INFORMATION: s is phosphorothioate linkage
197 <220> FEATURE:
198 <221> NAME/KEY: misc_feature
199 <222> LOCATION: (51)..(51)
200 <223> OTHER INFORMATION: s is phosphorothioate linkage
202 <220> FEATURE:
203 <221> NAME/KEY: misc_feature
204 <222> LOCATION: (53)..(53)

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205 <223> OTHER INFORMATION: s is phosphorothioate linkage
 207 <220> FEATURE:
 208 <221> NAME/KEY: misc_feature
 209 <222> LOCATION: (55)..(55)
 210 <223> OTHER INFORMATION: s is phosphorothioate linkage
 212 <220> FEATURE:
 213 <221> NAME/KEY: misc_feature
 214 <222> LOCATION: (57)..(57)
 215 <223> OTHER INFORMATION: s is phosphorothioate linkage
 217 <220> FEATURE:
 218 <221> NAME/KEY: misc_feature
 219 <222> LOCATION: (59)..(59)
 220 <223> OTHER INFORMATION: s is phosphorothioate linkage
 222 <220> FEATURE:
 223 <221> NAME/KEY: misc_feature
 224 <222> LOCATION: (61)..(61)
 225 <223> OTHER INFORMATION: s is phosphorothioate linkage
 227 <400> SEQUENCE: 8
 W--> 228 gccgnaacgg ccgnaccnan agngagncgn annaagccgg cnnngcacs a susgscscsg 60
 230 sgcaaugccg 70
 233 <210> SEQ ID NO: 9
 234 <211> LENGTH: 61
 235 <212> TYPE: DNA
 236 <213> ORGANISM: Artificial Sequence
 238 <220> FEATURE:
 239 <223> OTHER INFORMATION: Artificial oligonucleotide
 241 <400> SEQUENCE: 9
 242 ggatgcagca gcttstscctt gaagagcaaa ccggagacgt cgttgtagct agcctgcgtc 60
 244 a 61
 247 <210> SEQ ID NO: 10
 248 <211> LENGTH: 36
 249 <212> TYPE: DNA
 250 <213> ORGANISM: Artificial Sequence
 252 <220> FEATURE:
 253 <223> OTHER INFORMATION: Artificial primer
 255 <400> SEQUENCE: 10
 256 ctctggtggt ctggggcact gcacccctgac gcagaa 36
 259 <210> SEQ ID NO: 11
 260 <211> LENGTH: 32
 261 <212> TYPE: RNA
 262 <213> ORGANISM: Mus musculus
 264 <400> SEQUENCE: 11
 265 ggcuccggca ugugcaaagc cggcuucgcg gg 32
 268 <210> SEQ ID NO: 12
 269 <211> LENGTH: 81
 270 <212> TYPE: DNA
 271 <213> ORGANISM: Artificial Sequence
 273 <220> FEATURE:
 274 <223> OTHER INFORMATION: Synthetic extension product

RAW SEQUENCE LISTING

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PATENT APPLICATION: US/10/531,848

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Input Set : A:\Sequence Listing.ST25.txt

Output Set: N:\CRF4\08152006\J531848.raw

276 <400> SEQUENCE: 12
277 gacgcaggct agctacaacg acgtctccgg catgtgcaaa gccggcttgt tgacgcaggc 60
279 tagctacaac gacgtctccg g 81
282 <210> SEQ ID NO: 13
283 <211> LENGTH: 30
284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:
288 <223> OTHER INFORMATION: Artificial (DNAzyme)
290 <400> SEQUENCE: 13
291 gacgcaggct agctacaacg acgtctccgg
294 <210> SEQ ID NO: 14
295 <211> LENGTH: 49
296 <212> TYPE: DNA
297 <213> ORGANISM: Homo sapiens
299 <400> SEQUENCE: 14
300 ttctggtttg ctcttcaaga aagctgtgcc ccagaacacc agagacctc 49
303 <210> SEQ ID NO: 15
304 <211> LENGTH: 22
305 <212> TYPE: RNA
306 <213> ORGANISM: Mus musculus
308 <400> SEQUENCE: 15
309 ccggcaugug caaagccggc uu 22
312 <210> SEQ ID NO: 16
313 <211> LENGTH: 24
314 <212> TYPE: DNA
315 <213> ORGANISM: Homo sapiens
317 <400> SEQUENCE: 16
318 ggagacgtcg ttgtagctag cctg 24

*what is its source?
see item 11
on Enn summary
sheet*

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\Sequence Listing.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 77

Seq#:5; N Pos. 43

Seq#:6; N Pos. 43

Seq#:8; N Pos. 5, 14, 18, 20, 23, 27, 30, 32, 33, 42, 43, 44

VERIFICATION SUMMARY

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L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:60
L:108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0